

SEQUENCE LISTING

<110> BOYNTON, John  
GILLHAM, Nicholas  
RANDOLPH-ANDERSON, Barbara  
ISHIGE, Fumiharu  
SATO, Ryo

<120> METHODS OF CONFERRING PPO-INHIBITING HERBICIDE RESISTANCE IN PLANTS BY  
GENE MANIPULATION

<130> 2185-156P

<140> US 09/331,723

<141> 1999-08-18

<150> PCT/US96/20415

<151> 1996-12-27

<160> 24

<170> PatentIn version 3.0

<210> 1

<211> 47

<212> PRT

<213> Chlamydomonas reinhardtii

<220>

<221> misc\_feature

<223> Strain CC-407

<220>

<221> PEPTIDE

<222> (1)..(47)

<223> product = porphyrin herbicide resistance domain

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Thr	Leu	Ser	Tyr	Pro	Leu	Ser	Ala	Val	Arg	Glu	Glu	Arg	Lys	Ala	Ser
			20					25					30		
Asp	Gly	Ser	Val	Pro	Gly	Phe	Gly	Gln	Leu	His	Pro	Arg	Thr	Gln	
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<210> 2

<211> 46

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc\_feature

<223> ecotype Columbia

<220>

<221> PEPTIDE

<222> (1)..(46)

<223> product = porphyrin herbicide resistance domain

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Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val  
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 Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln  
 35 40 45

<210> 3  
 <211> 46  
 <212> PRT  
 <213> Zea mays

<220>  
 <221> misc\_feature  
 <223> Strain B73 inbred

<220>  
 <221> PEPTIDE  
 <222> (1)..(46)  
 <223> product = porphyric herbicide resistance domain

<400> 3  
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 1 5 10 15  
 Thr Val Ser Tyr Pro Lys Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp  
 20 25 30  
 Gly Glu Leu Gln Gly Phe Gly Gln Leu His Pro Arg Ser Gln  
 35 40 45

<210> 4  
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 <212> DNA  
 <213> Chlamydomonas reinhardtii

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 <222> (1)..(141)  
 <223> encodes porphyric herbicide resistance domain

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 gccgccgagg ccctgggctc ctgcgactac ccgccggtgg gcgccgtgac gctgtcgtag 60  
 ccgctgagcg ccgtgcggga ggagcgcaag gcctcggaac ggtccgtgcc gggcttcggt 120  
 cagctgcacc cgcgcacgca g 141

<210> 5  
 <211> 138  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> misc\_feature  
 <223> ecotype Columbia

<220>  
 <221> misc\_feature

<222> (1)..(138)  
 <223> encodes porphyric herbicide resistance domain

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 gctgcaaattg cactctcaaa actatattac ccaccagttg cagcagtatc tatctcgtac 60  
 ccgaaagaag caatccgaac agaattgttg atagatggtg aactaaaggg ttttgggcaa 120  
 ttgcatccac gcacgcaa 138

<210> 6  
 <211> 138  
 <212> DNA  
 <213> Zea mays

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 <223> Strain B73 inbred

<220>  
 <221> misc\_feature  
 <222> (1)..(138)  
 <223> encodes porphyric herbicide resistance domain

<400> 6  
 gctgcagatg ctctatcaag attctattat ccaccggttg ctgctgtaac tgtttcgtat 60  
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 ttgcatccac gtagtcaa 138

<210> 7  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 <222> (1)..(36)  
 <223> Oligonucleotide primer for Arabidopsis thaliana

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 ctatattacc caccaatggc agcagtatct atctcg 36

<210> 8  
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 <212> DNA  
 <213> Artificial Sequence

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 <222> (1)..(38)  
 <223> Oligonucleotide primer for Zea mays

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 gattctatta tccaccgatg gctgctgtaa ctgtttcg 38

<210> 9  
 <211> 26  
 <212> DNA

<213> Artificial Sequence

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<222> (1)..(26)

<223> Oligonucleotide primer common to both of *A. thaliana* and *Z. mays* porphyrinic herbicide resistance domain of PP

<220>

<221> misc\_feature

<222> (1)..(26)

<223> "n" residues can be inosine in addition to G, A, T or C; "k" at position 1 is equal to G or T; "y" at positions 3 and 6 is equal to C or T; "s" at positions 17 and 26 is equal to C or G; and "w" at position 25 is equal to A or T

<400> 9

kaytayccnc cnatggsngc ngtnws

26

<210> 10

<211> 2573

<212> DNA

<213> *Chlamydomonas reinhardtii*

<220>

<221> misc\_feature

<223> Strain RS-3

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<221> misc\_feature

<222> (1)..(2573)

<223> encodes protoporphyrinogen oxidase

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tccatcccga	ttccatccgc	tcctcctccc	ccacctagac	tgtctaccgt	ctaccagttt	180
cttgggcaat	cattaacgta	accccgccctc	cctgcgcctg	cccctccctc	cctctccccc	240
ccgcacagcc	cgccgcccgc	gaggccctgg	gctccttcga	ctaccgcgcg	atgggcgccc	300
tgacgctgtc	gtacccgctg	agcgccgtgc	gggaggagcg	caaggcctcg	gacgggtccg	360
tgccgggctt	cggtcagctg	cacccgcgca	cgcaggtggg	caagtgcgcg	cgtgttgccg	420
gcggtgtgtt	gcggaggggg	gggtggtggg	gggtgggggt	gggggtgggg	gggattgggg	480
cgctgggtcg	tatcccgcgg	ttgtatcctc	gcgctccctc	catccattcc	ccccttcaac	540
aacacacacg	ggcgcacacg	cacctctttt	gcgcttactt	tgtctggtgc	tccttaacac	600
actcttcgct	tcatttttgt	gtctttctaac	acacacactt	gtccacacac	agggcatcac	660
cactctgggc	accatctaca	gctccagcct	gttccccggc	cgcgcgcccg	agggccacat	720
gctgctgctc	aactacatcg	gcggcaccac	caaccgcggc	atcgtaacc	agaccaccga	780
gcagctggtg	gagcaggtgt	gtgtgtgggg	gggtgggggg	ggggcagtg	atttttgggc	840
tgagccccct	gagcaaagcg	atccaggggg	ggcgaaagccc	cccaggattg	cccctgtccg	900
tgcgtgcgtg	tgtgcctgtg	tcgacaaaaa	gtaccgtact	ggcaciaaac	gcgagtgcc	960
cgtattatta	attgcaatta	cctattgtag	aaaaatagac	ggcagggaaa	actcggccgg	1020
agcgagaagc	gacctcgtga	gtccatggac	atcttgactt	tcttcagttc	gcgagtatat	1080
ctctcgggcc	ctaaatatct	tacatccatg	tatcaaaaaca	tgtcgacgac	aagcgtcttg	1140
gggcaagaat	gtcgaaattg	tttgcaacag	ccaaaccatg	cgtccccgag	ccttacatgt	1200
gtcgcggccc	gggatccccg	gcccagagccc	ggctagccct	ttgcggtgct	tgagtgggat	1260
gtgggtgagg	tgcatthtgg	atatcatgga	ccgtgaagtg	gcgtgggtaa	ggtggcgtgg	1320
cgtggcgggg	acagggcatg	tcggtgcctc	ggcacagcgt	tggcctagt	gccagtcccc	1380
ctggatgggc	ttgcaagggt	gctgttcatt	tcgcccgtgc	ccatcgtcac	atccccctgc	1440
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gtcttggacc	cgtgttgctt	cggagctggc	cagaaccccc	tgtgggcaca	cacacgcaca	1560
cacacacaca	cacacacaca	cacacacaca	cacacacaca	cacacacaca	cacacacaca	1620
cacacacaca	cacacacaca	cacacacaca	cacacacaca	cacattttcg	tcttgcagcc	1680
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ctgctctcac	cgcctctccc	cccacccccat	ctccctgcag	gtggacaagg	acctgcgcaa	1800
catggtcatc	aagcccgcag	cgcccaagcc	ccgtgtggtg	ggcgtgcgcg	tgtggccgcg	1860
cgccatcccc	caggtgtgag	ggcgcagcag	ccggagggat	gggctagatc	ctagtctctc	1920
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ccctcccaac	ctagccacct	ctccccggat	ttgggttcac	tcggttgact	tgtttttggg	2040
ttctggaatc	aacttcacct	gttgtatact	ttgctgcact	tctctgtacc	actctttgca	2100
ttaggttcgg	tttagtttgg	gctgcatgtg	taaccctcc	tccccgccct	gccacctgca	2160
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cgcgggcgat	gattccttga	ctattgggac	ctatttcggt	gggctcgggc	acatgacccc	2520
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<210> 11  
 <211> 1704  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> misc\_feature  
 <223> ecotype Columbia

<220>  
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 <222> (16)..(1629)  
 <223> product = protoporphyrinogen oxidase

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		Met	Glu	Leu	Ser	Leu	Leu	Arg	Pro	Thr	Thr	Gln	Ser			
		1				5						10				
ctt	ctt	ccg	tcg	ttt	tcg	aag	ccc	aat	ctc	cga	tta	aat	ggt	tat	aag	99
Leu	Leu	Pro	Ser	Phe	Ser	Lys	Pro	Asn	Leu	Arg	Leu	Asn	Val	Tyr	Lys	
		15					20					25				
cct	ctt	aga	ctc	cgt	tgt	tca	gtg	gcc	ggt	gga	cca	acc	gtc	gga	tct	147
Pro	Leu	Arg	Leu	Arg	Cys	Ser	Val	Ala	Gly	Gly	Pro	Thr	Val	Gly	Ser	
		30				35				40						
tca	aaa	atc	gaa	ggc	gga	gga	ggc	acc	acc	atc	acg	acg	gat	tgt	gtg	195
Ser	Lys	Ile	Glu	Gly	Gly	Gly	Gly	Thr	Thr	Ile	Thr	Thr	Asp	Cys	Val	
	45			50			55			60						
att	gtc	ggc	gga	ggt	att	agt	ggt	ctt	tgc	atc	gct	cag	gcg	ctt	gct	243
Ile	Val	Gly	Gly	Gly	Ile	Ser	Gly	Leu	Cys	Ile	Ala	Gln	Ala	Leu	Ala	
		65					70			75						
act	aag	cat	cct	gat	gct	gct	ccg	aat	tta	att	gtg	acc	gag	gct	aag	291
Thr	Lys	His	Pro	Asp	Ala	Ala	Pro	Asn	Leu	Ile	Val	Thr	Glu	Ala	Lys	
		80					85			90						
gat	cgt	ggt	gga	ggc	aac	att	atc	act	cgt	gaa	gag	aat	ggt	ttt	ctc	339
Asp	Arg	Val	Gly	Gly	Asn	Ile	Ile	Thr	Arg	Glu	Glu	Asn	Gly	Phe	Leu	
		95				100				105						
tgg	gaa	gaa	ggt	ccc	aat	agt	ttt	caa	ccg	tct	gat	cct	atg	ctc	act	387
Trp	Glu	Glu	Gly	Pro	Asn	Ser	Phe	Gln	Pro	Ser	Asp	Pro	Met	Leu	Thr	
		110				115				120						
atg	gtg	gta	gat	agt	ggt	ttg	aag	gat	gat	ttg	gtg	ttg	gga	gat	cct	435

Met	Val	Val	Asp	Ser	Gly	Leu	Lys	Asp	Asp	Leu	Val	Leu	Gly	Asp	Pro		
125					130					135					140		
act	gcg	cca	agg	ttt	gtg	ttg	tgg	aat	ggg	aaa	ttg	agg	ccg	ggt	cca	483	
Thr	Ala	Pro	Arg	Phe	Val	Leu	Trp	Asn	Gly	Lys	Leu	Arg	Pro	Val	Pro		
				145					150					155			
tcg	aag	cta	aca	gac	tta	ccg	ttc	ttt	gat	ttg	atg	agt	att	ggt	ggg	531	
Ser	Lys	Leu	Thr	Asp	Leu	Pro	Phe	Phe	Asp	Leu	Met	Ser	Ile	Gly	Gly		
			160					165					170				
aag	att	aga	gct	ggt	ttt	ggt	gca	ctt	ggc	att	cga	ccg	tca	cct	cca	579	
Lys	Ile	Arg	Ala	Gly	Phe	Gly	Ala	Leu	Gly	Ile	Arg	Pro	Ser	Pro	Pro		
		175					180					185					
ggt	cgt	gaa	gaa	tct	gtg	gag	gag	ttt	gta	cgg	cgt	aac	ctc	ggt	gat	627	
Gly	Arg	Glu	Glu	Ser	Val	Glu	Glu	Phe	Val	Arg	Arg	Asn	Leu	Gly	Asp		
	190				195				200								
gag	ggt	ttt	gag	cgc	ctg	att	gaa	ccg	ttt	tgt	tca	ggt	ggt	tat	gct	675	
Glu	Val	Phe	Glu	Arg	Leu	Ile	Glu	Pro	Phe	Cys	Ser	Gly	Val	Tyr	Ala		
205				210				215						220			
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Lys	Leu	Glu	Gln	Asn	Gly	Gly	Ser	Ile	Ile	Gly	Gly	Thr	Phe	Lys	Ala		
			240				245					250					
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Ile	Gln	Glu	Arg	Lys	Asn	Ala	Pro	Lys	Ala	Glu	Arg	Asp	Pro	Arg	Leu		
		255				260						265					
cca	aaa	cca	cag	ggc	caa	aca	ggt	tct	ttc	agg	aag	gga	ctt	cga		867	
Pro	Lys	Pro	Gln	Gly	Gln	Thr	Val	Gly	Ser	Phe	Arg	Lys	Gly	Leu	Arg		
	270				275					280							
atg	ttg	cca	gaa	gca	ata	tct	gca	aga	tta	ggt	agc	aaa	ggt	aag	ttg	915	
Met	Leu	Pro	Glu	Ala	Ile	Ser	Ala	Arg	Leu	Gly	Ser	Lys	Val	Lys	Leu		
285				290				295						300			
tct	tgg	aag	ctc	tca	ggt	atc	act	aag	ctg	gag	agc	gga	gga	tac	aac	963	
Ser	Trp	Lys	Leu	Ser	Gly	Ile	Thr	Lys	Leu	Glu	Ser	Gly	Gly	Tyr	Asn		
			305				310							315			
tta	aca	tat	gag	act	cca	gat	ggt	tta	ggt	tcc	gtg	cag	agc	aaa	agt	1011	
Leu	Thr	Tyr	Glu	Thr	Pro	Asp	Gly	Leu	Val	Ser	Val	Gln	Ser	Lys	Ser		
		320					325					330					
ggt	gta	atg	acg	gtg	cca	tct	cat	ggt	gca	agt	ggt	ctc	ttg	cgc	cct	1059	
Val	Val	Met	Thr	Val	Pro	Ser	His	Val	Ala	Ser	Gly	Leu	Leu	Arg	Pro		
		335				340						345					
ctt	tct	gaa	tct	gct	gca	aat	gca	ctc	tca	aaa	cta	tat	tac	cca	cca	1107	
Leu	Ser	Glu	Ser	Ala	Ala	Asn	Ala	Leu	Ser	Lys	Leu	Tyr	Tyr	Pro	Pro		
	350				355					360							
ggt	gca	gca	gta	tct	atc	tcg	tac	ccg	aaa	gaa	gca	atc	cga	aca	gaa	1155	
Val	Ala	Ala	Val	Ser	Ile	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg	Thr	Glu		
365				370				375						380			
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Cys	Leu	Ile	Asp	Gly	Glu	Leu	Lys	Gly	Phe	Gly	Gln	Leu	His	Pro	Arg		
			385					390						395			
acg	caa	gga	ggt	gaa	aca	tta	gga	act	atc	tac	agc	tcc	tca	ctc	ttt	1251	
Thr	Gln	Gly	Val	Glu	Thr	Leu	Gly	Thr	Ile	Tyr	Ser	Ser	Ser	Leu	Phe		
		400					405						410				
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Pro	Asn	Arg	Ala	Pro	Pro	Gly	Arg	Ile	Leu	Leu	Leu	Asn	Tyr	Ile	Gly		
		415				420						425					
ggg	tct	aca	aac	acc	gga	att	ctg	tcc	aag	tct	gaa	ggt	gag	tta	gtg	1347	
Gly	Ser	Thr	Asn	Thr	Gly	Ile	Leu	Ser	Lys	Ser	Glu	Gly	Glu	Leu	Val		
	430				435						440						
gaa	gca	ggt	gac	aga	gat	ttg	agg	aaa	atg	cta	att	aag	cct	aat	tcg	1395	



Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly Lys Ile Arg Ala  
 165 170 175  
 Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro Gly Arg Glu Glu  
 180 185 190  
 Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp Glu Val Phe Glu  
 195 200 205  
 Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser  
 210 215 220  
 Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Gln  
 225 230 235 240  
 Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Gln Glu Arg  
 245 250 255  
 Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu Pro Lys Pro Gln  
 260 265 270  
 Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Glu  
 275 280 285  
 Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu Ser Trp Lys Leu  
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 Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn Leu Thr Tyr Glu  
 305 310 315 320  
 Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser Val Val Met Thr  
 325 330 335  
 Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro Leu Ser Glu Ser  
 340 345 350  
 Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val  
 355 360 365  
 Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp  
 370 375 380  
 Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val  
 385 390 395 400  
 Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala  
 405 410 415  
 Pro Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly Gly Ser Thr Asn  
 420 425 430  
 Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val Glu Ala Val Asp  
 435 440 445  
 Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser Thr Asp Pro Leu  
 450 455 460  
 Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val  
 465 470 475 480



Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser Leu Thr Ser Ser  
 485 490 495

Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ala Gly Val Ala  
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<210> 13  
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<220>  
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 <223> product = protoporphyrinogen oxidase

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 acc gcg cag gcg ctg gcc acg cgg cac ggc gtc ggg gac gtg ctt gtc 97  
 Thr Ala Gln Ala Leu Ala Thr Arg His Gly Val Gly Asp Val Leu Val  
 20 25 30  
 acg gag gcc cgc gcc cgc ccc ggc ggc aac att acc acc gtc gag cgc 145  
 Thr Glu Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg  
 35 40 45  
 ccc gag gaa ggg tac ctc tgg gag gag ggt ccc aac agc ttc cag ccc 193  
 Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro  
 50 55 60  
 tcc gac ccc gtt ctc acc atg gcc gtg gac agc gga ctg aag gat gac 241  
 Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp  
 65 70 75 80  
 ttg gtt ttt ggg gac cca aac gcg ccg cgt ttc gtg ctg tgg gag ggg 289  
 Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly  
 85 90 95  
 aag ctg agg ccc gtg cca tcc aag ccc gcc gac ctc ccg ttc ttc gat 337  
 Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp  
 100 105 110  
 ctc atg agc atc cca ggg aag ctc agg gcc ggt cta ggc gcg ctt ggc 385  
 Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly  
 115 120 125  
 atc cgc ccg cct cct cca ggc cgc gaa gag tca gtg gag gag ttc gtg 433  
 Ile Arg Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val  
 130 135 140  
 cgc cgc aac ctc ggt gct gag gtc ttt gag cgc ctc att gag cct ttc 481  
 Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe  
 145 150 155 160  
 tgc tca ggt gtc tat gct ggt gat cct tct aag ctc agc atg aag gct 529

Cys	Ser	Gly	Val	Tyr	Ala	Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala		
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Trp	Pro	Gln	Ala	Ile	Pro	Gln	Phe	Leu	Val	Gly	His	Leu	Asp	Leu	Leu		
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Ala Tyr Lys

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35 40 45

Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro  
50 55 60

Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp  
65 70 75 80

Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly  
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Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp  
100 105 110

Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly  
115 120 125

Ile Arg Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val  
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Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe  
145 150 155 160

Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala  
165 170 175

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Gly Gly Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys Pro  
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Phe Arg Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu  
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 Ser Val Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala  
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 Ser Asn Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu Ser  
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 Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys  
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